## REMARKS

**The Rejection of Claims 59-85 and 91 Under 35 U.S.C. §112, First Paragraph**

Claims 59-85 and 91 are rejected as containing new matter, i.e., subject matter not described in the application as filed. The particular recitations which are the focus of the rejection are:

- "comprising a first number of pieces enumerated within one of said windows" (claims 59 and 75; emphasis added)
- "comprising a first number of pieces enumerated within a window." (claim 91; emphasis added)

The emphasis indicates the disputed portion of the recitation.

The PTO asserts that the comparing of pieces within an individual window is not disclosed. Applicant respectfully traverses. The specification discloses:

> The sequence tags in the population are enumerated to determine the number of individual sequence tags present in the population. The number of a plurality of sequence tags in the population is compared to the number of the plurality of sequence tags determined for a genome of a reference cell. The plurality of sequence tags are within a window of sequence tags which are calculated to be contiguous in the genome of the species of the eukaryotic cell. A difference in the number of the plurality of sequence tags within the window present in the population from the number determined for a reference eukaryotic cell indicates a karyotypic difference between the test eukaryotic cell and the reference eukaryotic cell.

(Specification at paragraph 6; emphasis added) Thus the specification discloses comparing the number of tags within a window to identify a difference in the number of tags within the window. Because the method of the invention is useful as a genome-wide analysis (see [17]) typically many such comparisons would be performed. The claims are open to comparing in one

or more windows.

The originally filed specification provides additional support for the recitations in current claim 59-85 and 91 at originally filed claims 1 and 37 which recite, "comparing the number of a plurality of sequence tags...wherein the plurality of sequence tags are within a window of sequence tags..." (emphasis added).

Thus the originally filed application discloses comparisons within a single window. Therefore it is respectfully submitted that these recitations do not constitute impermissible new matter. Withdrawal of this rejection is respectfully requested.

**The Rejection of Claims 1-24, 30-34, 37-58, and 86-89 Under 35 U.S.C. §112, Second Paragraph**

Claim 1 has been amended to clarify its meaning, without changing the scope of the claims. As the examiner correctly surmised, the intended meaning of the prior recitation ("number which is a sum of numbers of a plurality of") was "number of copies." The claim as amended reflects this intended meaning.

Claim 37 has been similarly amended for clarity purposes only.

Claims 1, 37, and 86-89 have been amended to recite that the test eukaryotic cell and the reference eukaryotic cell are of the same species. Species refers to a taxonomic classification, as in the phrase "genus and species." Two human cells are of the same species, *i.e., Homo sapiens*. It is respectfully submitted that this terminology is clear and known to those of skill in the art.

Withdrawal of this rejection is respectfully requested.

**The Rejection of Claims 25-36 Under 35 U.S.C. §102(b) and/or §103(a)**

The rejected claims have been cancelled to expedite allowance of the application. This rejection is therefore moot.

**The Rejection of Claims 37-38, 42, 47-50, 52, 56, and 58 Under 35 U.S.C. §103(a)**

Claims 37-38, 42, 47-50, 52, 56, and 58 are rejected as unpatentable over U.S. 6,498,013 (Velculescu) in view of Dunn. This rejection is respectfully traversed.

The rejected claims comprise independent claim 37 and dependent claims 38, 42, 47-50, 52, 56, and 58, which are dependent from claim 37.

Velculescu is cited for teaching long SAGE technique in which RNA expression is analyzed by making sequence tags, dimerizing them, concatenating them, and enumerating them. Moreover, Velculescu is cited as teaching enumeration of less than 100% of the sequence tags in Example 1. (col. 15, lines 30-67).

Dunn is cited as teaching generation of sequence tags from genomic DNA. The rejection posits that it would have been obvious for one or ordinary skill in the art to modify the method of Velculescu to use genomic DNA, as taught by Dunn.

This rejection must fail because it fails to teach all elements of the claim. It is fundamental that a *prima facie* case of obviousness must provide prior art teachings which cumulatively demonstrate all elements of the claimed invention.

> To establish a *prima facie* case of obviousness, three basic criteria must be met. First, there must be some suggestion or motivation, either in the references themselves or in the knowledge generally available to one of ordinary skill in the art, to modify the reference or to combine reference teachings. Second, there must be a reasonable expectation of success. ***Finally, the prior art reference (or references when combined) must***

***teach or suggest all the claim limitations.***

M.P.E.P. §2143, emphasis added. The applied combination of references fails to teach the step of comparing a first number of copies of a plurality of sequence tags to a second number of copies of said plurality of sequence tags, where *the plurality of sequence tags are within a window of sequence tags which are calculated to be contiguous in the genome.*

The most recent Office Action (mailed May 17, 2006) does not specifically address this limitation, but the prior Office Action (mailed November 16 2005) does. The prior Office Action asserts that Dunn's concatamerized, dimerized tags comprising 10-50 tags "read on a window of sequence tags comprising 10 to 500, and 50 to 1000 contiguous tags." Office Action of November 16, 2005, at page 9, lines 1-5.

However, the tags in a clone of concatamerized, dimerized tags are not tags which are calculated to be contiguous in the genome. The dimers and the concatamers are ***randomly*** joined, and thus their order or their presence in a clone provides no information about their contiguity in the genome.

The Office Action of November 16, 2005 further asserts that Dunn teaches "enumerating the pieces of a plurality of windows for the test cell to pieces for a reference cell." Page 10, lines 12-19, citing Dunn at page 1763, col. 1, third paragraph. However, Dunn does not explicitly or implicitly teach the use of windows. Dunn teaches:

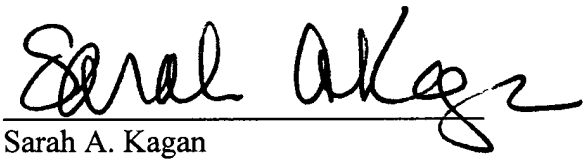
> In summary, the basic GST procedure described here provides a means for genome-wide fingerprinting of chromosomal and episomal DNAs and, by extension, for profiling DNA genomes in natural populations. Like SAGE, it can be performed with equipment available in most molecular biology laboratories. The GST technique can be used,

with minor modifications, for long SAGE analysis of eukaryotic mRNAs and might, like AFLP of cDNA (Qin et al. 2001♦; Donson et al. 2002♦), be adaptable for profiling gene expression in prokaryotes.

Thus, neither Dunn nor Velculescu teach the use of a window, *i.e.*, a plurality of pieces of genomic DNA which are calculated to be contiguous in the genome of the reference eukaryotic cell. Since no cited reference provides this teaching, the *prima facie* case must fail.

Respectfully submitted,

Dated: November 15, 2006

By: 

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